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1600

RAW SEQUENCE LISTING

DATE: 03/14/2003

PATENT APPLICATION: US/09/612,894

TIME: 08:05:20

Input Set : N:\Crf3\RULE60\09612894.RAW.txt

Output Set: N:\CRF4\03142003\I612894.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

(i) APPLICANT: Stocco, Douglas M.

Clark, Dr. Barbara J.

(ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATION
OF STEROIDOGENESIS

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Akir, Gump, Strauss, Bauer & Feld, L.L.P.

(B) STREET: 1901 Frost Bank Plaza, 916 Congress Avenue

(C) CITY: Austin

(D) STATE: TX

(E) COUNTRY: U.S.A.

(F) ZIP: 78701

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/09/612,894

(B) FILING DATE: 27-Feb-2001

(C) CLASSIFICATION: 530

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/658,284

(B) FILING DATE: 07-JUN-1996

(A) APPLICATION NUMBER: US 08/538,960

(B) FILING DATE: 04-OCT-1995

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mayfield, Denise L.

(B) REGISTRATION NUMBER: 33,732

(C) REFERENCE/LOCKET NUMBER: 48301,0000

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 512/499-6200

(B) TELEFAX: 512/499-6296

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: 7085 "TGA"

C--> 28

C--> 29

W--> 35

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63      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64      GTGACCCAC GGGTCCGCTC AGGAGCTTGA AAGGCTCAGG AAGAACAACC CTGAGCACC      60
65      TCAGCACTCA GCATGTTCCT CGCTAGTTTC AAGCTGTGTG CTGGAAGCTC CTATAGCAT      120
66      ATGCGGAATA TGAAGGATT AAGGCAACAA GGTGTCTGTG CCATTGGCCA AGAGCTCAAC      180
67      TGGAGAGGAC TGGGGATTTC CAGTCCCGGG TGGATGGGTC AAGTTCGAGC TGGAGCTCT      240
68      CTGCTTGGTT CTCAGCTTGA ACGAATCTTC TAACTTACC ACGAGCTGTC CTACATCCAC      300
69      CAGGGAGAGT TGGTATPDA GAAGGCTTTC GGCATATPCA ACAACCAAGA AGGCTTGAAG      360
70      AAGAAAGGCT ATGATGAA CAAGGATGAA GTGCTAGGTA AATATGCTTC AATATGCTTC      420
71      AAGGTGTTTC GGTGGAATCT GTTCTTACAC CAGGCGATTC ACAGACCTTA TGAGGAAGTT      480
72      TGGGACCGGA TGGAGGATAT TGGAGATGTC AAGCCAAATC TCAAGGAGAT CAAGGTCTCTG      540
73      CAGAGGATTC GAAAGAGATC GGTTCATGACT CATGAGCTGC CTGCGCGCGGC AGCAGGCAAC      600
74      CTGCTGGGGC CTCAGAGATT CTGAGGCTTC CGCTGTACCA AGGCGAGAGG TTCCACCTGT      660
75      TGTCTGGGAC GCATGCTTAC AATTTTGGG GAGATCGCGG AGCAGAGTGG TGCAATCAGA      720
76      GCTGAACAGC GCGCGAGCTC CATGCTGCTT CATCCACTGC CTGGAAGTCC CTCCAAGACT      780
77      AAAGTCACTT GGTGCTGCTC TATTGAGCTG AAGGCTTGGC TGCGGAAGAG AATCATCAAC      840
78      CAGGTCTTAT CCAAGCTCA CATAGAGTTC GCGCAAGTAC TGCGCAAGCG CCTGGAAGCC      900
79      AGGCTCTGCT CTCAGAGTCA GGTGTAAGGA CTGCTTACCA CATGAGCTTC CAAATCATTC      960
80      GAAGCTCTCA CAGGAGGCT TAAAGTCTG CCATCTTCAG CTAACAGCAT CCGGAGGGGT      1020
81      GGTAGTCA ATAGATCTAG AATGACTGAT AAAATAGGA TAGCAAAAT AGAAATGAGG      1080
82      CTAGAAATAA AATGCTCTTA GTGCTCTCA CTGATAGCT TGGAGGGCTA AGGATAAGT      1140
83      AGCTADGAAA CTTTCTTCT AGGTCTTCT ATGCTGAGCT AAAAGACATC AGTATCTAGC      1200
84      AACAGGGGAT GCTAAATATC GCGAATCTTC GTCTTACCAG CTCCAAATCT CACTACCTGA      1260
85      AGGCACTCTG CACACAGAGC AAGGTCTTTC CTAGGAAACT CTGTAAAAGT TCTCTCTGT      1320
86      AAAAGGCGAG AACTTCTAG AAGTACCTA CAAAGGGGCT TTCCAGAGTA TTCCAAGTTT      1380
87      TCTCTGAGGA GAAATGAAAC CATCATTTGT CCGACTTCCC TACTAATCCC ATGACAATAA      1440
88      AGAACATACA TAAAAAATAA AAAAAA      1466

```

115 (2) INFORMATION FOR SEQ ID NO: 2:

116 (i) SEQUENCE CHARACTERISTICS:

117 (A) LENGTH: 176 amino acids

118 (B) TYPE: amino acid

119 (C) STRANDEDNESS: single

120 (D) TOPOLOGY: linear

121 (ii) MOLECULE TYPE: protein

122 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

123 Met Phe Leu Ala Thr Phe Lys Leu Lys Ala Gly Ser Ser Tyr Arg His
124 1 5 10 15
125 Met Arg Asn Met Lys Gly Leu Arg His Gln Ala Val Leu Ala Ile Gly
126 20 25 30
127 Gln Glu Leu Asn Trp Arg Ala Leu Gly Asp Ser Ser Pro Gly Trp Met
128 35 40 45
129 Gly Gln Val Arg Arg Arg Ser Ser Leu Leu Gly Ser Gln Leu Glu Ala
130 50 55 60
131 Thr Leu Tyr Ser Asp Gln Gln Leu Ser Tyr Ile Gln Gln Gly Gln Val
132 65 70 75 80
133 Ala Met Gln Lys Ala Leu Gly Ile Leu Asn Asn Gln Glu Gly Trp Lys
134 85 90 95
135 Lys Gln Ser Thr Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
136 100 105 110 115
137 Pro Asp Val Gly Lys Val Phe Arg Leu Glu Val Val Val Asp Gln Pro

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151      115      120      135
154 Met Asp Arg Leu Tyr Glu Glu Leu Val Asp Arg Met Glu Ala Met Gly
155      135      135      140
157 Glu Trp Asn Pro Asn Val Lys Glu Ile Lys Val Leu Gln Arg Ile Gly
158      145      150      155      160
160 Lys Asp Thr Val Ile Thr His Glu Leu Ala Ala Ala Ala Ala Gly Asn
161      165      170      175
163 Leu Met Gly Pro Arg Asn Thr Val Ser Val Arg Cys Thr Lys Arg Arg
164      175      180      190
166 Gly Ser Thr Cys Val Leu Ala Gly Met Ala Thr His Phe Gly Glu Met
167      195      200      205
169 Pro Glu Gln Ser Gly Val Ile Arg Ala Glu His Gly Pro Thr Cys Met
170      210      215      220
172 Val Leu His Pro Leu Ala Gly Ser Pro Ser Lys Thr Lys Leu Thr Trp
173      225      230      235      240
175 Leu Leu Ser Ile Asp Leu Lys Gly Trp Leu Pro Lys Thr Ile Ile Asn
176      245      250      255
178 Glu Val Leu Ser Gln Thr Gln Ile Glu Phe Ala Asn His Leu Arg Lys
179      260      265      270
181 Arg Leu Glu Ala
182      275

```

181 (2) INFORMATION FOR SEQ ID NO: 1:

182 (i) SEQUENCE CHARACTERISTICS:

183 (A) LENGTH: 14 amino acids

184 (B) TYPE: amino acid

185 (C) STRANDEDNESS: single

186 (D) TOPOLOGY: linear

187 (ii) MOLECULE TYPE: peptide

188 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

189 Ala Glu His Gly Pro Thr Cys Met Val Leu His Pro Leu Ala

190 1 5 10

191 (2) INFORMATION FOR SEQ ID NO: 4:

192 (i) SEQUENCE CHARACTERISTICS:

193 (A) LENGTH: 12 amino acids

194 (B) TYPE: amino acid

195 (C) STRANDEDNESS: single

196 (D) TOPOLOGY: linear

197 (ii) MOLECULE TYPE: peptide

198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

199 Ala Leu Gly Ile Leu Asn Asn Gln Glu Gly Trp Lys

200 1 5 10

201 (2) INFORMATION FOR SEQ ID NO: 5:

202 (i) SEQUENCE CHARACTERISTICS:

203 (A) LENGTH: 3 amino acids

204 (B) TYPE: amino acid

205 (C) STRANDEDNESS: single

206 (D) TOPOLOGY: linear

207 (ii) MOLECULE TYPE: peptide

208 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

RAW SEQUENCE LISTING

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235      Gly Ser Thr Cys Val Leu Ala Gly Met Ala Thr His Phe Gly Glu Met
236      1             5             10             15
238      Pro Glu Gln
241 (2) INFORMATION FOR SEQ ID NO: 6:
242      (i) SEQUENCE CHARACTERISTICS:
243          (A) LENGTH: 6 amino acids
244          (B) TYPE: amino acid
245          (C) STRANDEDNESS: single
246          (D) TOPOLOGY: linear
247      (ii) MOLECULE TYPE: peptide
248      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
249      Asn Glu Glu Gly Trp Lys
250      1             5
251 (2) INFORMATION FOR SEQ ID NO: 7:
252      (i) SEQUENCE CHARACTERISTICS:
253          (A) LENGTH: 9 amino acids
254          (B) TYPE: amino acid
255          (C) STRANDEDNESS: single
256          (D) TOPOLOGY: linear
257      (ii) MOLECULE TYPE: peptide
258      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
259      Ala Glu His Ser Pro Thr Cys Met Val
260      1             5
261 (2) INFORMATION FOR SEQ ID NO: 8:
262      (i) SEQUENCE CHARACTERISTICS:
263          (A) LENGTH: 11 amino acids
264          (B) TYPE: amino acid
265          (C) STRANDEDNESS: single
266          (D) TOPOLOGY: linear
267      (ii) MOLECULE TYPE: peptide
268      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
269      Ile Leu Asn Asn Gln Glu Gly Trp Lys Lys Glu
270      1             5             10
271 (2) INFORMATION FOR SEQ ID NO: 9:
272      (i) SEQUENCE CHARACTERISTICS:
273          (A) LENGTH: 25 base pairs
274          (B) TYPE: nucleic acid
275          (C) STRANDEDNESS: single
276          (D) TOPOLOGY: linear
277      (ii) MOLECULE TYPE: other nucleic acid
278      (A) DESCRIPTION: 5'-seq = "TNA"
279      (ix) FEATURE:
280          (A) NAME KEY: mod_fied_base
281          (B) LOCATION: 10-13, 17, 18, 19
282          (D) OTHER INFORMATION: /mod_base= OTHER
283 /note "N = (A or C or G or T/U) or (unknown or other)"
284 /x= 5'-seq:
285      (A) NAME KEY: modified base
286      (B) LOCATION: 6

```

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Output Set: N:\CRF4\03142003\I612894.raw

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316          (D) OTHER INFORMATION: /mod_base= OTHER
317 /note= "R = A or G"
318      (ix) FEATURE:
319          (A) NAME/KEY: modified_base
320          (B) LOCATION: chr-01(9, 21)
321          (D) OTHER INFORMATION: /mod_base= OTHER
322 /note= "S = C or T"
323      (xi) SEQUENCE INFORMATION: SEQ ID NO: 9:
324 GCGGARGCAYG GNC GACGTCG YAT AG
325 (2) INFORMATION FOR SEQ ID NO: 10:
326      (i) SEQUENCE CHARACTERISTICS:
327          (A) LENGTH: 25 base pairs
328          (B) TYPE: nucleic acid
329          (C) STRANDEDNESS: single
330          (D) TOPOLOGY: linear
331      (ii) MOLECULE TYPE: other nucleic acid
332          (A) DESCRIPTION: /desc = "DNA"
333      (ix) FEATURE:
334          (A) NAME/KEY: modified_base
335          (B) LOCATION: chr-01(8, 17)
336          (D) OTHER INFORMATION: /mod_base= OTHER
337 /note= "R = A or G"
338      (ix) FEATURE:
339          (A) NAME/KEY: modified_base
340          (B) LOCATION: chr-01(8, 11, 14, 23)
341          (D) OTHER INFORMATION: /mod_base= OTHER
342 /note= "N = (A or C or G or T/U) or (unknown or other)"
343      (ix) FEATURE:
344          (A) NAME/KEY: modified_base
345          (B) LOCATION: 18
346          (D) OTHER INFORMATION: /mod_base= OTHER
347 /note= "Y = C or T/U"
348      (xi) SEQUENCE INFORMATION: SEQ ID NO: 10:
349 CCATRCAGC" NGGCGGCGCY TCGC
350 (2) INFORMATION FOR SEQ ID NO: 11:
351      (i) SEQUENCE CHARACTERISTICS:
352          (A) LENGTH: 17 basepairs
353          (B) TYPE: nucleic acid
354          (C) STRANDEDNESS: single
355          (D) TOPOLOGY: linear
356      (ii) MOLECULE TYPE: other nucleic acid
357          (A) DESCRIPTION: /desc = "DNA"
358      (ix) FEATURE:
359          (A) NAME/KEY: modified_base
360          (B) LOCATION: 5
361          (D) OTHER INFORMATION: /mod base= OTHER
362 /note= "Y = C or T/U"
363      (ix) FEATURE:
364          (A) NAME/KEY: modified base

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/612,894

DATE: 03/14/2003

TIME: 08:05:21

Input Set : N:\Crf3\RULE60\09612894.RAW.txt

Output Set: N:\CRF4\03142003\I612894.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:35 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)